

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:00 ; Search time 755.06 Seconds  
(without alignments)  
26.115 Million cell updates/sec

Title: US-09-851-670-14

Perfect score: 23  
Sequence: 1 gagaacacccgcctctgcgaac 23

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N.GeneSeq\_1101: \*  
1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT: \*  
2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT: \*  
3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT: \*  
4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT: \*  
5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT: \*  
6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT: \*  
7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT: \*  
8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT: \*  
9: /SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT: \*  
10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT: \*  
11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT: \*  
12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT: \*  
13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT: \*  
14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT: \*  
15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT: \*  
16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT: \*  
17: /SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT: \*  
18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT: \*  
19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT: \*  
20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT: \*  
21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT: \*  
22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 14.6  | 63.5        | 50     | 16    | AAO88993    |
| 2          | 14    | 60.9        | 40     | 14    | AAO38058    |
| 3          | 13.6  | 59.1        | 27     | 19    | AAV63948    |
| 4          | 13.6  | 59.1        | 27     | 20    | AAV63948    |
| 5          | 13.2  | 57.4        | 30     | 16    | AAO3746     |
| 6          | 13    | 56.5        | 24     | 19    | AAV43655    |
| 7          | 13    | 56.5        | 34     | 21    | AAZ87445    |
| 8          | 13    | 56.5        | 34     | 21    | AAZ90126    |
| 9          | 13    | 56.5        | 58     | 18    | AAV6207     |
| 10         | 12.8  | 55.7        | 20     | 20    | AAV3589     |
| 11         | 12.6  | 54.8        | 20     | 22    | AAO1329     |

|   |    |      |      |    |    |          |                    |
|---|----|------|------|----|----|----------|--------------------|
| C | 12 | 12.6 | 54.8 | 27 | 22 | AAH40207 | SNP specific SNPE  |
| C | 13 | 12.6 | 54.8 | 27 | 22 | AAH70982 | Ligand 21A-ts. Un  |
| C | 14 | 12.6 | 54.8 | 35 | 20 | AAH81412 | PCR primer EI used |
| C | 15 | 12.6 | 54.8 | 39 | 14 | AAQ36898 | RG678, a mutagenic |
| C | 16 | 12.4 | 53.9 | 20 | 21 | AAQ41824 | Baculovirus C2 com |
| C | 17 | 12.4 | 53.9 | 20 | 21 | AAZ73223 | Human biallelic ma |
| C | 18 | 12.4 | 53.9 | 26 | 20 | AAH76977 | PCR primer for his |
| C | 19 | 12.4 | 53.9 | 31 | 22 | AAI30851 | Human single nucle |
| C | 20 | 12.4 | 53.9 | 34 | 15 | AAO73465 | Porcine interleuk1 |
| C | 21 | 12.4 | 53.9 | 41 | 15 | AAO73468 | Porcine interleuk1 |
| C | 22 | 12.4 | 53.9 | 51 | 22 | AAH38608 | Human SNP flanking |
| C | 23 | 12.2 | 53.0 | 21 | 20 | AAZ35959 | Human Wnt1 PCR pri |
| C | 24 | 12.2 | 53.0 | 21 | 22 | AAO80402 | Internal transcrib |
| C | 25 | 12.2 | 53.0 | 24 | 21 | AAZ95736 | Barley empty donor |
| C | 26 | 12.2 | 53.0 | 25 | 21 | AAZ59161 | Primer #2 for huma |
| C | 27 | 12.2 | 53.0 | 30 | 16 | AAO89021 | VEGF 2'-NH2-RNA nu |
| C | 28 | 12.2 | 53.0 | 40 | 17 | AAH69463 | Plasmid p182Sflr c |
| C | 29 | 12.2 | 53.0 | 40 | 17 | AAH69463 | Plasmid p182Sflr c |
| C | 30 | 12.2 | 53.0 | 40 | 20 | AAH88887 | Circular plasmid e |
| C | 31 | 12.2 | 53.0 | 40 | 20 | AAH88893 | Circular plasmid e |
| C | 32 | 12.2 | 53.0 | 43 | 20 | AAH18868 | Maize SSR oligonuc |
| C | 33 | 12.2 | 53.0 | 43 | 20 | AAH18871 | Maize SSR oligonuc |
| C | 34 | 12.2 | 53.0 | 43 | 20 | AAH18874 | Maize SSR oligonuc |
| C | 35 | 12.2 | 53.0 | 44 | 21 | AAH75400 | Fragment derived f |
| C | 36 | 12.2 | 53.0 | 50 | 20 | AAH52072 | Synthetic plasmid  |
| C | 37 | 12   | 52.2 | 20 | 15 | AAO74652 | Aspergillus aculea |
| C | 38 | 12   | 52.2 | 25 | 15 | AAV38473 | Human CC chemokine |
| C | 39 | 12   | 52.2 | 26 | 16 | AAO98435 | Truncated 2'-NH2 b |
| C | 40 | 12   | 52.2 | 26 | 16 | AAO98439 | Control oligo, deo |
| C | 41 | 12   | 52.2 | 26 | 18 | AAO98438 | Truncated bGCF RNA |
| C | 42 | 12   | 52.2 | 26 | 22 | AAH65452 | Basic fibroblast g |
| C | 43 | 12   | 52.2 | 26 | 22 | AAH70724 | Oligonucleotide #1 |
| C | 44 | 12   | 52.2 | 26 | 22 | AAH70983 | Control ligand deo |
| C | 45 | 12   | 52.2 | 27 | 20 | AAH81123 | PCR primer for clo |

#### ALIGNMENTS

|          |   |                                |
|----------|---|--------------------------------|
| RESULT 1 | AAO88993/C  | AAO88993 standard; RNA: 50 BP. |
| ID       | AAO88993;   |                                |
| AC       | AAO88993;   |                                |
| DT       | 28-SEP-1995   | (first entry)                  |
| DE       | VEGF 2'-NH2-RNA nucleic acid ligand family 2, oligo 23b.          |                                |
| XX       |   |                                |
| KW       | Nucleic acid; ligand; thrombin; elastase; rheophylline; caffeine; |                                |
| KW       | pharmaceutical; diagnosis; vascular endothelial growth factor;    |                                |
| KW       | gene therapy; RNA; DNA; ss.                                       |                                |
| OS       | Synthetic.  |                                |
| FT       | Key   | Location/Qualifiers            |
| FT       | modified_base   | 1                              |
| FT       | /*tag= a  | /note= "2'-NH2-Cytosine"       |
| PN       | W09507364-A.  |                                |
| XX       |   |                                |
| PD       | 16-MAR-1995.  |                                |
| XX       |   |                                |
| PF       | 08-SEP-1994;  | 94WO-US10306.                  |
| XX       |   |                                |
| PR       | 08-SEP-1993;  | 93US-011791.                   |
| PR       | 07-OCT-1993;  | 93US-0134028.                  |
| PR       | 22-FEB-1994;  | 94US-0199507.                  |
| PR       | 25-APR-1994;  | 94US-0233012.                  |
| PR       | 28-APR-1994;  | 94US-0234997.                  |
| XX       |   |                                |
| PA       | (NEXA-) NEXAGEN INC.  |                                |

XX Biesecker G, Gold L, Janjic N, Jayasena S, Jenison RD;  
PI Kirschenheuter GP, Pieken W, Polisky B, Smith D, Tasset D;  
DR WPI: 1995-123436/16.  
XX  
XX  
PT Identifying nucleic acid ligands for target molecules - by  
PT partitioning increased affinity nucleic acids from a candidate  
PT mixt. and amplifying  
XX  
XX  
PS Claim 37: Fig 34; 251pp; English.  
XX  
XX  
CC The sequences given in AAQ88993-98 represent nucleic acid ligands to  
CC vascular endothelial growth factor (VEGF). These ligands all  
CC contain the consensus sequence given in AAQ88999. These ligands were  
CC identified using the method of the invention. The method comprises  
CC contacting a candidate mixture with the target molecule (i.e. VEGF)  
CC where the nucleic acids which have an increased affinity to the target  
CC relative to the candidate mixture can be partitioned from the remainder  
CC of the candidate mixture. The increased affinity nucleic acids are  
CC partitioned from the remainder of the candidate mixture and the isolated  
CC nucleic acids are amplified to yield a ligand-enriched mixture of  
CC nucleic acids, in which the nucleic acid ligands can be identified.  
CC The isolated ligands may be used as pharmaceuticals, diagnostic agents  
CC and in gene therapy. The ligands may be RNA or DNA molecules.  
XX  
XX  
SQ Sequence 50 BP; 11 A; 12 C; 19 G; 8 U; 0 other;

Query Match 63.5%; Score 14.6; DB 16; Length 50;  
Best Local Similarity 81.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 agaacacccgcctctcgcgcaa 22  
IIIIII IIIIIII IIII  
DB 28 AGACACCCCGCTCTGTGTGTA 8

RESULT 2  
AAQ38058  
ID AAQ38058 standard; DNA; 40 BP.  
XX  
XX  
AC AAQ38058;  
XX  
XX  
DT 07-JUL-1993 (first entry)  
XX  
XX  
DE Oligonucleotide gel15, for produ. of synthetic gelonin gene.  
XX  
XX  
KW Seed: toxin; plant; cloning; ribosomal; protein synthesis; ss;  
KW Gelonium multiflorum.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN WO9305168-A.  
XX  
XX  
PD 18-MAR-1993.  
XX  
XX  
PE 21-AUG-1992; 92WO-US07066.  
XX  
XX  
PR 06-SEP-1991; 91US-0755949.  
XX  
XX  
PA (RERE-) RES DEV FOUND.  
XX  
XX  
PI Beattie KL, Rosenblum MG;  
XX  
XX  
DR WPI: 1993-100990/12.  
XX  
XX  
PT Synthetic DNA encoding gelonin plant toxin - provides nucleotide  
PT sequence for synthetic gene for produ. and cloning  
XX  
XX  
PS Example 4; Fig 5; 45pp; English.  
XX  
XX  
CC The synthetic gelonin gene based on the sequence of Gelonium

CC multiflorum gelonin was prepd. by synthesizing a number of  
CC oligonucleotides corresp. to fragments of the gelonin gene and  
CC annealing and ligating to assemble the intact gene. The  
CC oligonucleotides were designed to contain a codon triplet for each  
CC amino acid in the corresp. gelonin fragment. Gelonin is a ribosomal-  
CC inactivating plant toxin which inhibits protein synthesis. The  
CC synthetic form of gelonin provides a plentiful, reproducible source  
CC of gelonin which may be modified.  
CC See also AAQ38041-82.  
XX  
XX  
SQ Sequence 40 BP; 12 A; 14 C; 7 G; 7 T; 0 other;

Query Match 60.9%; Score 14; DB 14; Length 40;  
Best Local Similarity 77.3%; Pred. No. 6.5e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacacccgcctctcgcgcaa 23  
I IIIII IIIII I III  
DB 17 acacacccatctctcgcgaaa 38

RESULT 3  
AAV63948  
ID AAV63948 standard; DNA; 27 BP.  
XX  
XX  
AC AAV63948;  
XX  
XX  
DT 21-JAN-1999 (first entry)  
XX  
XX  
DE Mycobacterium tuberculosis sensu oligonucleotide pVR3.  
XX  
XX  
KW Mycobacterium tuberculosis; antigen; vaccine; immunological;  
KW Immunogen; infection; primer; ss.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN WO9844119-A1.  
XX  
XX  
PD 08-OCT-1998.  
XX  
XX  
PE 01-APR-1998; 98WO-DK00132.  
XX  
XX  
PR 05-JAN-1998; 98US-0070488.  
PR 02-APR-1997; 97DK-0000375.  
PR 18-APR-1997; 97US-0044624.  
PR 10-NOV-1997; 97DK-0001277.  
XX  
XX  
PA (STAT-) STATENS SERUM INST.  
XX  
XX  
PI Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB;  
PI Rosenkrands I, Weidigh K;  
XX  
XX  
DR WPI: 1998-542705/46.  
XX  
XX  
PT New isolated mycobacteria polypeptides and nucleic acids - used for  
PT developing products for the diagnosis of or vaccination against  
PT mycobacterial infections, particularly tuberculosis  
XX  
XX  
PS Example 2; Page 52; 163pp; English.  
XX  
XX  
CC The present sequence represents an oligonucleotide used in an example  
CC from the present invention. Products from the present invention, which  
CC describes protein fragments and nucleic acid fragments derived from  
CC M. tuberculosis, can be used in the detection of and prevention of  
CC mycobacterial infections. In particular, the proteins and nucleic acids  
CC can be used for the diagnosis of or vaccination against tuberculosis  
CC caused by M. tuberculosis, M. africanum or M. bovis.  
XX  
XX  
SQ Sequence 27 BP; 8 A; 8 C; 7 G; 4 T; 0 other;

|                       |   |                    |           |            |
|-----------------------|---|--------------------|-----------|------------|
| Query Match           | 59.1%;  | Score 13.6;        | DB 20;    | Length 27; |
| Best Local Similarity | 80.0%;  | Pred. No. 9.7e+02; |           |            |
| Matches 16;           | Conservative 0;   | Mismatches 4;      | Indels 0; | Gaps 0;    |
| OY                    | 4 aacaccgcgtctctcgcaaa 23   |                    |           |            |
| Db                    | 3 aacaccgcggatgctcgcaaa 22  |                    |           |            |
| RESULT 5              |   |                    |           |            |
| AAAT03746             |   |                    |           |            |
| ID                    | AAAT03746 standard; cDNA; 30 BP.  |                    |           |            |
| XX                    |   |                    |           |            |
| AC                    | AAAT03746;  |                    |           |            |
| XX                    |   |                    |           |            |
| DT                    | 28-MAR-1996 (first entry)   |                    |           |            |
| XX                    |   |                    |           |            |
| DE                    | PCR primer for amplifying gax gene.   |                    |           |            |
| XX                    |   |                    |           |            |
| KW                    | Gax: smooth muscle cell; proliferation; inhibition; gene therapy; atheromatous plaque; balloon angioplasty; artery; ss. |                    |           |            |
| KW                    |   |                    |           |            |
| OS                    | Synthetic.  |                    |           |            |
| XX                    |   |                    |           |            |
| PN                    | W09523161-A1.   |                    |           |            |
| PD                    | 31-AUG-1995.  |                    |           |            |
| XX                    |   |                    |           |            |
| PF                    | 22-FEB-1995; 95WO-US01882.  |                    |           |            |
| XX                    |   |                    |           |            |
| PR                    | 24-FEB-1994; 94US-0203532.  |                    |           |            |
| XX                    |   |                    |           |            |
| PA                    | (UYCA-) UNIV CASE WESTERN RESERVE.  |                    |           |            |
| XX                    |   |                    |           |            |
| PI                    | Gorski DH, Walsh K;   |                    |           |            |
| XX                    |   |                    |           |            |
| DR                    | WPI; 1995-311500/40.  |                    |           |            |
| XX                    |   |                    |           |            |
| PT                    | Rat and human growth arresting homeo-box gene - inhibits vascular   |                    |           |            |
| PT                    | smooth muscle cell growth, useful in treatment of blood vessel  |                    |           |            |
| PT                    | diseases  |                    |           |            |
| XX                    |   |                    |           |            |
| PS                    |   |                    |           |            |
| XX                    |   |                    |           |            |
| XX                    | Disclosure; Page 16; 48pp; English.   |                    |           |            |
| CC                    | The Gax protein (AAR82096 (rat) or AAR82097 (human)) can be used for  |                    |           |            |
| CC                    | inhibiting the proliferation of eukaryotic cells, esp. vascular smooth  |                    |           |            |
| CC                    | muscle cell proliferation by gene therapy. The gax gene (AAAT03744  |                    |           |            |
| CC                    | (rat) or AAAT03745 (human)) or fragment of it may be administered to  |                    |           |            |
| CC                    | the interior wall during balloon angioplasty to inhibit the   |                    |           |            |
| CC                    | proliferation of vascular smooth muscle cells and reduce the chances  |                    |           |            |
| CC                    | of the formation of atheromatous plaques and internal arterial  |                    |           |            |
| CC                    | thickening. Two primers (AAAT03746, AAAT03747) were used to amplify the   |                    |           |            |
| CC                    | coding region of the gax cDNA spanning nucleotides 200-1108 for its   |                    |           |            |
| CC                    | subcloning into an expression vector and the production of a  |                    |           |            |
| CC                    | Glutathione-S-transferase-Gax fusion protein.   |                    |           |            |
| XX                    |   |                    |           |            |
| SQ                    | Sequence 30 BP; 4 A; 13 C; 8 G; 5 T; 0 other;   |                    |           |            |
| Query Match           | 57.4%;  | Score 13.2;        | DB 16;    | Length 30; |
| Best Local Similarity | 83.3%;  | Pred. No. 1.6e+03; |           |            |
| Matches 15;           | Conservative 0;   | Mismatches 3;      | Indels 0; | Gaps 0;    |
| OY                    | 3 gaacaccgcgtctctcgc 20   |                    |           |            |
| Db                    | 13 gaacaccgcgtcttggc 30   |                    |           |            |
| RESULT 6              |   |                    |           |            |
| AAV43655              |   |                    |           |            |
| ID                    | AAV43655 standard; DNA; 24 BP.  |                    |           |            |

XX AAV43655;  
AC XX  
DT 28-SEP-1998 (first entry)  
XX  
DE Detection probe used in target-triggered amplification.  
XX  
KM Promoter sequestered oligonucleoside; CPS; RNA polymerase promoter;  
KW target-triggered amplification; probe; ss.  
XX  
OS Synthetic.  
OS Bacteriophage t7.  
XX  
PN EP851033-A1.  
XX  
PD 01-JUL-1998.  
XX  
PF 23-DEC-1997; 97EP-0310550.  
XX  
PR 30-DEC-1996; 96US-0770941.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Becker MM, Myers KK, Stull PD;  
XX WPI; 1998-335379/30.  
XX  
DR Promoter-sequestered oligonucleoside used in trigger amplification  
PT of nucleic acid - comprises complementary first and second nucleic  
PT acid sequences and single-stranded loop containing RNA polymerase  
PT promoter  
XX  
PS Example 1; Page 13; 39pp; English.  
XX  
CC The present sequence represents a detection probe used to exemplify  
CC the method of invention. The invention provides promoter-sequestered  
CC oligonucleoside which has a stem comprising first and second nucleic  
CC acid sequences, which are substantially complementary to each other and  
CC a single-stranded loop region located between the first and second  
CC sequence, where all, or a portion, of an RNA polymerase promoter  
CC sequence is located within the loop region. The promoter-sequestered  
CC oligonucleoside is used in trigger amplification of a nucleic acid  
CC comprising the target sequence, under amplifying conditions, forming a  
CC functional double-stranded promoter region and producing multiple copies  
CC of nucleic acid using the target sequence or the target complementary  
CC sequence as a template under RNA polymerase mediated amplification  
CC conditions. It can also detect the nucleic acid sequence, by combining  
CC it and the sample, under amplifying conditions, forming a functional  
CC double-stranded promoter region if the target sequence is present in  
CC the sample, producing RNA transcripts under RNA polymerase mediated  
CC amplification conditions using the functional promoter and detecting  
CC whether RNA transcripts are produced.  
XX  
SO Sequence 24 BP; 8 A; 9 C; 3 G; 4 T; 0 other;

Query Match 56.5%; Score 13; DB 19; Length 24;  
Best Local Similarity 76.2%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaaccgcgtctctcgaa 22  
Db 2 agaaccgcgtctctcgaa 22

RESULT 7  
AAZ87445  
ID AAZ87445 standard; DNA; 34 BP.  
XX  
AC AAZ87445;  
XX  
DT 22-MAY-2000 (first entry)

XX  
DE  
XX  
KM Polypeptide; macrocyclic biosynthesis; polypeptide synthase; PKS;  
KW multienzyme complex; loading module; ketosynthase domain; KS; CLF domain;  
KW decarboxylation; acyl carrier protein domain; ACP; anthelmintic;  
KW insecticide; immunosuppressant; antifungal; antibacterial; spiramycin;  
KW hybrid PKS; PCR primer; ss.  
XX  
OS Streptomyces ambofaciens.  
XX  
PN WO200000618-A2.  
XX  
PD 06-JAN-2000.  
XX  
PF 29-JUN-1999; 99WO-GB02044.  
XX  
PR 29-JUN-1998; 98GB-0014006.  
XX  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
XX  
PI Leadlay PF, Staunton J, Cortes J, McArthur HAI;  
XX WPI; 2000-170919/15.  
XX  
DR Novel methods for preparing new variant polypeptides, for use as  
PT anthelmintics, insecticides, immunosuppressants, antifungals or  
PT antibacterials  
XX  
PS Example 16; Page 53; 97pp; English.  
XX  
CC The invention relates to a novel system for producing polypeptides  
CC particularly 12-, 14- and 16-membered ring macrocyclics from a desired  
CC starter unit. The biosynthesis of polypeptides is initiated by a group  
CC of chain-forming enzymes known as polypeptide synthases (PKSs) which are  
CC multi-enzyme complexes consisting of a set, or module, of enzymes  
CC which catalyse polypeptide chain extension. The system of the  
CC invention comprises inserting loading modules into PKSs that do not  
CC normally possess them, thereby controlling the starter units used. The  
CC loading module may be adapted to load an optionally substituted malonyl  
CC residue, which it then decarboxylates to provide an optionally  
CC substituted acetyl residue for transfer to a chain extension module. The  
CC loading module comprises a KS (ketosynthase)-type domain which effects  
CC decarboxylation, and an acyl carrier protein domain (ACP). The KS-type  
CC domain is preferably a Ksq domain, which possesses a glutamine rather  
CC than a cysteine in the active site. Alternatively a CLF-type domain,  
CC which also contains a glutamine at this site, may provide the  
CC decarboxylating functionality. The methods of the invention are used to  
CC produce polypeptides, particularly 12-, 14- and 16-membered ring  
CC macrocyclics. The system is used to produce macrocyclics with preferred  
CC (acetate or propionate) starter units, or with unusual starter units,  
CC which minimises the formation of by-products containing a different  
CC starter unit. The polypeptides produced have use as potential  
CC antibiotics, insecticides, immunosuppressants, antifungals or  
CC antibacterials. The present invention provides a system for producing  
CC polypeptides which minimises the formation of by-products containing an  
CC undesired or different starter units, and also allows the incorporation  
CC of unusual starter units. The system allows the identification of  
CC polypeptides which may have enhanced properties or possess novel  
CC bioactivities. Sequences AAZ87437-287456 represent PCR primers used in  
CC exemplifications of the present invention to amplify DNA encoding  
CC PKS functional domains of a variety of actinomycetes. The amplified  
CC DNA was then used in the construction of genes encoding hybrid  
CC polypeptide synthases.  
XX  
SO Sequence 34 BP; 7 A; 10 C; 8 G; 9 T; 0 other;

Query Match 56.5%; Score 13; DB 21; Length 34;  
Best Local Similarity 76.2%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 gagaaccgcgtctctcgaa 21

Db 12 gagactcgcgattccgcga 32  
||||| | | | | | | |

RESULT 8

AA290126  
ID AA290126 standard; DNA; 34 BP.

AC AA290126;

DT 19-MAY-2000 (first entry)

DE PCR primer for amplifying a spiramycin producing PKS gene fragment.

KW 14-member macrolide; spiramycin-producing loading module; antibiotic;

OS Streptomycetes ambofaciens.

PN WO200000500-A2.

PD 06-JAN-2000.

PE 29-JUN-1999; 99WO-GB02042.

PR 29-JUN-1998; 98GB-0014006.

PA (BIOT-) BIOTICA TECHNOLOGY LTD.

PA (PRIZ ) PRIZER INC.

PI Leadlay PF, Staunton J, Cortes J, McArthur HAI;

DR WPI: 2000-170901/15.

PT New 14-member macrolides incorporating acetate starter unit, used as

PS antibiotics -

PS Example 8; Page 38; 78pp; English.

CC This sequence represents a PCR primer used to amplify the  
CC spiramycin-producing loading module from the Streptomycetes ambofaciens  
CC polyketide synthase (PKS) genes. PKS is used in a system for the  
CC production of the macrolides of the invention. The macrolides are  
CC 14-member macrolides that incorporate an acetate starter unit so that it  
CC has a 13-methyl substituent, provided that it is not norethromycin C,  
CC 6-deoxy-15-norethromycin B or 6-deoxy-15-norethromycin D. The new  
CC 14-member macrolides may be used as antibiotics. The macrolides are  
CC produced by a process which minimizes the formation of by-products  
CC containing different starter units. 13-Methyl erythromycins can be  
CC produced at good expression levels and in substantial absence of  
CC erythromycins with different starter units. Chemical modifications  
CC previously only possible with 'natural' erythromycins can be performed.

Sequence 34 BP; 7 A; 10 C; 8 G; 9 T; 0 other;

Query Match 56.5%; Score 13; DB 21; Length 34;

Best Local Similarity 76.2%; Pred. No. 2e+03;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 gagaacaccgcgtctctcgca 21  
||||| | | | | | | |

Db 12 gagaacaccgcgtctctcgca 32

RESULT 9

AAV76207/C

ID AAV76207 standard; DNA; 58 BP.

AC AAV76207;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #1896.

KW Computer readable medium; vaccine; S.aureus infection; immunodetection;

KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KW skin infection; surgical wound infection; scalded skin syndrome;

OS Staphylococcus aureus.

PN EP786519-A2.

PD 30-JUL-1997.

PE 07-JAN-1997; 97EP-0100117.

PR 05-JAN-1996; 96US-0009861.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

DR WPI: 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines

PS Claim 1; Page 2089; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
CC computer readable medium.

Sequence 58 BP; 6 A; 14 C; 19 G; 19 T; 0 other;

Query Match 56.5%; Score 13; DB 18; Length 58;

Best Local Similarity 76.2%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 gaacaccgcgtctctcgcaaa 23  
||||| | | | | | | |

Db 33 GAACACCACGCTGCGCAAA 13

RESULT 10

AA33589

ID AA33589 standard; DNA; 20 BP.

AC AA33589;

DT 09-JUL-1999 (first entry)

DE Oligonucleotide tag 20-mer #5.

XX Labelling; tag; molecular species; identification; property;

KW characteristic; hybridisation; amplification; ss.

XX OS Synthetic.  
XX PN MO9918240-A2.  
XX PD 15-APR-1999.  
XX PF 05-OCT-1998; 98WO-US20874.  
XX PR 06-OCT-1997; 97US-0944410.  
XX PA (STRA-) STRATAGEME.  
XX PI Sorage JA;  
XX DR WPI; 1999-264040/22.  
XX PT Uniquely tagged molecules identifiable by a unique property or  
XX PT characteristic  
XX PS Disclosure: Page 45; 138pp; English.  
XX  
CC The present invention describes a composition comprising a mixture of  
CC different species of molecules where each species is linked to a tag  
CC that is unique to that species and that encodes at least two variable  
CC positions on that species, where the tags can be identified without the  
CC need for first isolating each of the tags prior to identification. Liquid  
CC phase hybridisation system may be used for simultaneous identification  
CC of a large subset of targets out of a very large collection of similar  
CC of dissimilar molecular species. It may also be used to create tagged  
CC molecules that identify any collection of molecular species, e.g.  
CC peptides, antibodies, nucleic acids. Method bar codes collections or  
CC probes or analytes for use in a liquid phase hybridisation method. Tagged  
CC probes able to detect small changes or mutations in the target specimen.  
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.  
CC the concentration of the probe would not be limited by the solid support,  
CC both the target nucleic acids and the probes can diffuse toward each  
CC other, and signal amplification through cycling reactions could occur.  
CC Sequencing DNA with tags in combination with DNA amplification techniques  
CC means that there is no need for traditional sequencing methods or  
CC attaching to a solid phase, either the materials to be analysed or the  
CC tags. The present sequence represents an oligonucleotide tag from the  
CC present invention.  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 other;  
XX  
Query Match 55.7%; Score 12.8; DB 20; Length 20;  
Best Local Similarity 87.5%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 acaccgcctctcgc 20  
    |||||  
DB 4 acactgcctcgcgc 19  
    |||||  
RESULT 11  
AADI1329  
ID AADI1329 standard; DNA: 20 BP.  
AC AADI1329;  
DT 24-SEP-2001 (first entry)  
XX Human cot oncogene antisense oligonucleotide, ISIS 116370.  
DE  
XX Human: cot oncogene; antisense therapy; inflammation: cancer; antisense;  
KW immune system disorder; prophylaxis: cytostatic; immunomodulator;  
KM Tpl-2; est: phosphorothioate backbone; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX

EH Key Location/Qualifiers  
FT modified\_base  
FT 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl residues"  
FT 5  
FT /\*tag= c  
FT /mod\_base= m5c  
FT 9  
FT /\*tag= d  
FT /mod\_base= m5c  
FT 10  
FT /\*tag= e  
FT /mod\_base= m5c  
FT 11  
FT /\*tag= f  
FT /mod\_base= m5c  
FT 13  
FT /\*tag= g  
FT /mod\_base= m5c  
FT 14  
FT /\*tag= h  
FT /mod\_base= m5c  
FT 15  
FT /\*tag= i  
FT /mod\_base= m5c  
FT 16..20  
FT /\*tag= j  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl residues"  
FT 17  
FT /\*tag= k  
FT /mod\_base= m5c  
FT 19  
FT /\*tag= l  
FT /mod\_base= m5c  
FT 20  
FT /\*tag= m  
FT /mod\_base= m5c  
XX  
XX US6265216-B1.  
XX  
XX 24-JUL-2001.  
XX PD  
XX 20-JAN-2000; 2000US-0489868.  
XX PE  
XX 20-JAN-2000; 2000US-0489868.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Bennett CF, Wyatt J;  
XX PI  
XX WPI; 2001-463936/50.  
XX  
XX Example 15; Column 41; 39pp; English.  
XX  
CC The invention relates to antisense oligonucleotides, compositions  
CC and methods for modulating cot oncogene expression. The cot oncogene  
CC is also known as Tpl-2 and est. The compositions comprise antisense  
CC compounds, particularly antisense oligonucleotides, targeted to  
CC nucleic acids encoding cot oncogene. The antisense oligonucleotides  
CC are useful for modulating the expression of cot oncogene and for  
CC treating diseases associated with expression of cot oncogene, e.g.  
CC inflammation, cancer or disorders of the immune system. The antisense

CC oligonucleotides are also useful for diagnosis or prophylaxis or as  
CC research reagents and kits. The present sequence is human cot oncogene  
CC antisense oligonucleotide, ISIS 116370. This sequence was targeted  
CC towards the coding region of human cot oncogene.  
CC  
XX

SO Sequence 20 BP; 5 A; 10 C; 3 G; 2 T; 0 other;

Query Match 54.8%; Score 12.6; DB 22; Length 20;  
Best Local Similarity 78.9%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 agaacacccgcctctcgc 20  
||||| ||| |||||  
Db 1 agaacagacccctcctcgc 19

RESULT 12  
AAH40207/c  
ID AAH40207 standard; DNA; 27 BP.

AC AAH40207;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 3003.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; primer; ss.

XX Homo sapiens.

OS WO200129262-A2.

PN 26-APR-2001.

PD 13-OCT-2000; 2000WO-US28436.

PF 15-OCT-1999; 99US-0160096.

PR (ORCH-) ORCHID BIOSCIENCES INC.

PA Picoult-Newburg L, Pohl M;

PI WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample -  
PT  
XX

PS Claim 1; Page 65; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer,  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial

CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence.  
CC  
XX

SO Sequence 27 BP; 4 A; 5 C; 11 G; 6 T; 1 other;

Query Match 54.8%; Score 12.6; DB 22; Length 27;  
Best Local Similarity 75.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacacccgcctctcgcga 21  
||||| ||| |||||  
Db 23 ACANCAACCGCATCTCGCA 4

RESULT 13  
AAF70982/c  
ID AAF70982 standard; DNA; 27 BP.

AC AAF70982;

DT 20-APR-2001 (first entry)

DE Ligand 21A-ts.

XX Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;  
KW atherosclerosis; angioplasty; stability; ss.

XX Unidentified.

OS US6177557-B1.

PN 23-JAN-2001.

PD 05-AUG-1996; 96US-0687421.

PF 11-JUN-1990; 90US-0536428.

PR 10-JUN-1991; 91US-0714131.

PR 06-NOV-1992; 92US-0973333.

PR 10-FEB-1994; 94US-0195005.

PR 28-MAR-1994; 94US-0219012.

PA (NEXS-) NEXSTAR PHARM INC.

PI Janjic N, Gold L, Tasset D;

PI WPI; 2001-158583/16.

XX Novel nucleic acid ligands to basic fibroblast growth factor that are  
PT useful as inhibitors of basic fibroblast growth factors and 2'-amino  
PT modified RNA ligands, exhibit increased in vivo stability -  
PT  
XX

PS Claim 1; Column 27; 153pp; English.

XX The present invention relates to a purified and isolated non-naturally  
CC occurring DNA ligands to basic fibroblast growth factor (bFGF).  
CC The ligands are useful as part of gene therapy treatments and  
CC for diagnosing pathogenesis of vascular diseases including  
CC initiation and progression of atherosclerosis, acute coronary  
CC syndromes, vein graft disease and restenosis following coronary  
CC angioplasty. The ligands have improved stability in vivo.  
CC  
XX

SO Sequence 27 BP; 4 A; 3 C; 13 G; 6 U; 1 other;

Query Match 54.8%; Score 12.6; DB 22; Length 27;  
Best Local Similarity 69.6%; Pred. No. 3e+03;  
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 gagagacacccgtctctcgcaaa 23  
 ||| ||||| ||| ||| |||  
 Db 27 GHAACACACCGCTGCTTCCACA 5

RESULT 14  
 AAX81412/c  
 ID AAX81412 standard; DNA: 35 BP.  
 XX AAX81412:

XX 25-AUG-1999 (first entry)

DE PCR primer E1 used to amplify a human airway trypsin protease intron.

XX Human airway trypsin protease; intron; disease predisposition;  
 KW polymorphism; respiratory disease; chronic obstructive pulmonary disease;  
 KW sinobronchial syndrome; pulmonary emphysema; diffuse bronchiolitis;  
 KW bronchiectasis; abnormal muco-cilia bio-defence system; PCR primer: ss.  
 XX

OS Synthetic.  
 OS Homo sapiens.

PN W0931271-A1.

PD 24-JUN-1999.

PF 16-DEC-1998; 98WO-JP05689.

PR 16-DEC-1997; 97JP-0346494.

PA (TEIJ ) TEIJIN LTD.

PI Eguchi H, Masuda K, Yamaoka K, Yasuoka S;

DR WPI: 1999-395192/33.

PT Human airway trypsin protease gene polymorphism-based prediction of  
 PT predisposition of individuals to specific diseases (claimed),  
 PT therapeutic effect or prognosis following treatments

PS Claim 5; Page 41; 55pp; Japanese.

CC PCR primers AAX81412-13 were used to amplify an intron of human airway  
 CC trypsin protease. The specification describes a method for prediction of  
 CC the predisposition of individuals to specific diseases, or therapeutic  
 CC effect on the patients or the prognosis following the treatments. The  
 CC method is based on the analysis of human airway trypsin protease gene  
 CC polymorphism. The method is used for diagnosis and therapy. The ability  
 CC to forecast relapse after treatment can be achieved by this method, as  
 CC well as the determination of predisposition of individuals to specific  
 CC diseases, e.g. respiratory diseases, including chronic obstructive  
 CC pulmonary disease, sinobronchial syndrome, pulmonary emphysema, diffuse  
 CC bronchiolitis and bronchiectasis. The methods can also be used for  
 CC diagnosis of abnormal muco-cilia bio-defence system.

SO Sequence 35 BP; 8 A; 2 C; 16 G; 9 T; 0 other;

Query Match 54.8%; Score 12.6; DB 20; Length 35;  
 Best Local Similarity 78.9%; Pred. No. 3.1e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 aacaccgctctctcgcaa 22  
 ||||| ||||| ||| |||  
 Db 35 AACATCGGCTCTCACACCA 17

RESULT 15  
 AAQ36898  
 ID AAQ36898 standard; DNA: 39 BP.  
 XX

AC AAQ36898;  
 XX  
 DT 15-JUN-1993 (first entry)  
 XX

DE RG678, a mutagenic PCR primer.

XX FPV; fowlpox virus; infectious bursal disease virus; IBV; vaccine;  
 KW Faragher; STC; TROVAC; VP2; ss.  
 XX

PN W09303145-A.

PD 18-FEB-1993.

PF 22-JUL-1992; 92WO-US06100.

PR 26-JUL-1991; 91US-0736254.

PA (VITRO-) VIROGENETICS CORP.

PI Gettig R, Paoletti E, Taylor J;

DR WPI: 1993-076502/09.

PT Recombinant pox-virus contg. infectious bursal disease virus DNA  
 PT - used to produce vaccines for providing protective immunity  
 PT against IBV infections, partic. in poultry

PS Example 10; Page 27; 67pp; English.

CC In order to change the VP2 Faragher sequence in pCEN120 to VP2 STC  
 CC sequence, five codons were changed in the VP2 ORF using PCR site  
 CC directed mutagenesis. Oligonucleotide primers RG677 plus RG678 and  
 CC RG685 plus RG686P were used to amplify a 530 bp and a 270 bp fragment  
 CC respectively from pCEN100. The gel purified 270 bp fragment was further  
 CC amplified using oligonucleotides RG702 and RG704. These purified  
 CC fragments which contain the five STC codon changes, were ligated into  
 CC pCEN120. The resulting plasmid, pVP2-STC was confirmed by DNA sequence  
 CC analysis. See also AAQ36873-906.  
 XX

SO Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 other;

Query Match 54.8%; Score 12.6; DB 14; Length 39;  
 Best Local Similarity 78.9%; Pred. No. 3.2e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 aacaccgctctctcgcaa 22  
 ||||| ||||| ||| |||  
 Db 3 aacacgagctctcccccaa 21

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